

CLAIMS

1. A method for separating a hepatic, endothelial, or hematopoietic progenitor cell from a cell population, wherein the method comprises the steps of:

- 5 a) detecting the expression of a WT1 gene in a cell in a cell population; and
 b) separating the cell in which expression of the WT1 gene was detected.

2. A method for simultaneously separating at least two progenitor cells from a cell population, wherein the progenitor cells are selected from hepatic, endothelial, and
10 hematopoietic progenitor cells, and wherein the method comprises the steps of:

 a) detecting the expression of a WT1 gene in a cell in a cell population comprising at least two progenitor cells, selected from hepatic, endothelial, and hematopoietic progenitor cells; and

- b) separating the cells in which expression of the WT1 gene was detected.

3. The method of claim 1 or 2, wherein expression of the WT1 gene is detected by using expression of a WT1 gene or of a reporter gene linked to a WT1 promoter as an indicator.

4. The method of claim 3, wherein the reporter gene is a lacZ gene or GFP gene, and
20 expression of the reporter gene is detected by a FACS assay.

5. The method of any one of claims 1 to 4, wherein a hepatic progenitor cell or an endothelial progenitor cell is separated when the expression level of the WT1 gene is in the range of $2.21 (\pm 1.62) \times 10^{-2}$ (when expression of the WT1 gene in a K562 leukemia cell line is defined as 1), and a hematopoietic progenitor cell is separated when the expression level of the WT1
25 gene is in the range of $3.54 (\pm 3.39) \times 10^{-4}$ (when expression of the WT1 gene in a K562 leukemia cell line is defined as 1).